STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/563,503_

Source: _TFWP_

Date Processed by STIC: _1-13-06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: |O|S63/SO3

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length

The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3_____Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4_____Non-ASCII

The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5_____Variable Length

Sequence(s)_____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7_____Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8_____Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
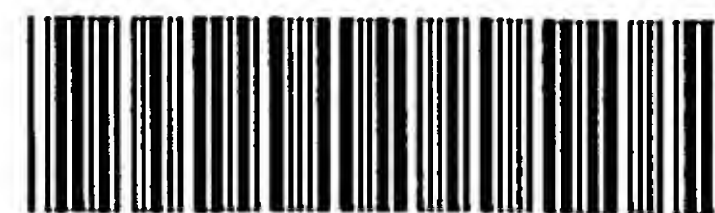<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue n or Xaa represents.

10_____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ✓ Misuse of n/Xaa

"n" can only represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

IFWP

RAW SEQUENCE LISTING   DATE: 01/13/2006
PATENT APPLICATION: US/10/563,503   TIME: 12:10:37

        Input Set : A:\pto.da.txt
        Output Set: N:\CRF4\01132006\J563503.raw

```
        5 <110> APPLICANT: Stordeur, Patrick
        6         Goldman, Michel
       10 <120> TITLE OF INVENTION: Device, kit and method for pulsing biological samples with
an agent and
       11         stabilising the sample so pulsed
       15 <130> FILE REFERENCE: DECLE35.005APC
C--> 19 <140> CURRENT APPLICATION NUMBER: US/10/563,503
C--> 20 <141> CURRENT FILING DATE: 2006-01-04
       22 <150> PRIOR APPLICATION NUMBER: PCT/EP03/07453
       24 <151> PRIOR FILING DATE: 2003-07-10
       28 <160> NUMBER OF SEQ ID NOS: 10
       32 <170> SOFTWARE: PatentIn version 3.1
       36 <210> SEQ ID NO: 1
       38 <211> LENGTH: 22
       40 <212> TYPE: DNA
       42 <213> ORGANISM: Homo sapiens
       46 <400> SEQUENCE: 1
       47 ctcaccagga tgctcacatt ta                              22
       48 <210> SEQ ID NO: 2
       50 <211> LENGTH: 24
       52 <212> TYPE: DNA
       54 <213> ORGANISM: Homo sapiens
       58 <400> SEQUENCE: 2
       59 tccagaggtt tgagttcttc ttct                            24
       60 <210> SEQ ID NO: 3
       62 <211> LENGTH: 25
       64 <212> TYPE: DNA
       66 <213> ORGANISM: Homo sapiens
       70 <220> FEATURE:
       72 <221> NAME/KEY: misc_feature
       74 <222> LOCATION: (1)..(1)
       76 <223> OTHER INFORMATION: N = 6Fam
       79 <220> FEATURE:
       81 <221> NAME/KEY: misc_feature
       83 <222> LOCATION: (25)..(25)
       85 <223> OTHER INFORMATION: N = Tamra-p
       88 <400> SEQUENCE: 3
W--> 89 ntgcccaaga aggccacaga actgn
       90 <210> SEQ ID NO: 4
       92 <211> LENGTH: 21
       94 <212> TYPE: DNA
       96 <213> ORGANISM: Homo sapiens
      100 <400> SEQUENCE: 4
      101 actttgaaca gcctcacaga g                               21
```

[handwritten annotations:] Does Not Comply / Corrected Diskette Needed → (Pg. 1-2)

[handwritten:] Invalid response

[handwritten:] ← pls see item #13 on error summary sheet.

```
         RAW SEQUENCE LISTING                  DATE: 01/13/2006
         PATENT APPLICATION:  US/10/563,503    TIME: 12:10:37

                   Input Set : A:\pto.da.txt
                   Output Set: N:\CRF4\01132006\J563503.raw

     102 <210> SEQ ID NO: 5
     104 <211> LENGTH: 20
     106 <212> TYPE: DNA
     108 <213> ORGANISM: Homo sapiens
     112 <400> SEQUENCE: 5
     113 ttggaggcag caaagatgtc                                        20
     114 <210> SEQ ID NO: 6
     116 <211> LENGTH: 23
     118 <212> TYPE: DNA
     120 <213> ORGANISM: Homo sapiens
     124 <220> FEATURE:
     126 <221> NAME/KEY: misc_feature
     128 <222> LOCATION: (1)..(1)
     130 <223> OTHER INFORMATION: N -(6Fam)
     133 <220> FEATURE:
     135 <221> NAME/KEY: misc_feature
     137 <222> LOCATION: (23)..(23)
     139 <223> OTHER INFORMATION: N =(Tamra-p)
     142 <400> SEQUENCE: 6
W--> 143 nctgtgcacc gagttgaccg tan                                   23
     144 <210> SEQ ID NO: 7
     146 <211> LENGTH: 22
     148 <212> TYPE: DNA
     150 <213> ORGANISM: Homo sapiens
     154 <400> SEQUENCE: 7
     155 tgtcacaaac agtgcaccta ct
     156 <210> SEQ ID NO: 8
     158 <211> LENGTH: 26
     160 <212> TYPE: DNA
     162 <213> ORGANISM: Homo sapiens
     166 <400> SEQUENCE: 8
     167 agttacaata ggtagcaaac cataca                                 26
     168 <210> SEQ ID NO: 9
     170 <211> LENGTH: 21
     172 <212> TYPE: DNA
     174 <213> ORGANISM: Homo sapiens
     178 <400> SEQUENCE: 9
     179 taattgcctc acattgtcac t                                      21
     180 <210> SEQ ID NO: 10
     182 <211> LENGTH: 21
     184 <212> TYPE: DNA
     186 <213> ORGANISM: Homo sapiens
     190 <400> SEQUENCE: 10
     191 attcagctcg aacactttga a                                      21
```

Invalid response

← See item #13 on error summary sheet.

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/13/2006
PATENT APPLICATION: US/10/563,503   TIME: 12:10:38

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\01132006\J563503.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 1,25
Seq#:6; N Pos. 1,23

VERIFICATION SUMMARY   DATE: 01/13/2006
PATENT APPLICATION: US/10/563,503   TIME: 12:10:38

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\01132006\J563503.raw**

```
L:19 M:270 C: Current Application Number differs, Replaced Application Number
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
```